

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 08:36:35 ; Search time 16.52 Seconds

(without alignments)
1198.873 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540
Sequence: 1 VYLSECKTGKNGKNYRGTMK.....TNSQVPMYCKIPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1535	99.7	810	1 PLHU	plasmin (EC 3.4.21
2	1442	93.6	810	2 B30848	plasmin (EC 3.4.21
3	1292	83.9	790	1 PLRC	plasmin (EC 3.4.21
4	1281	83.8	812	1 PLBO	plasmin (EC 3.4.21
5	1274	82.7	812	1 PLMS	plasmin (EC 3.4.21
6	1237	80.3	810	2 I46260	plasmin (EC 3.4.21
7	881	57.2	2869	2 T18518	hepatocyte growth
8	797	51.8	728	1 JH0579	hepatocyte growth
9	782	50.8	728	1 A35644	hepatocyte growth
10	776.5	50.4	710	1 I51283	hepatocyte growth
11	776	50.4	728	1 A60185	hepatocyte growth
12	766.5	49.8	716	1 JCS061	hepatocyte growth
13	754.5	49.0	411	2 I51285	hepatocyte growth
14	753.5	48.9	716	1 A40332	macrophage-stimula
15	749	48.6	4548	1 S00657	apoptosis (a) (EC
16	739	48.0	711	1 A47136	macrophage-stimula
17	739	48.0	1420	2 A32869	apoptosis (a) (EC
18	505	32.8	455	2 A61545	plasmin (EC 3.4.21
19	499	32.4	460	2 B61545	plasmin (EC 3.4.21
20	391.5	25.4	336	2 S33879	plasmin precursor
21	372	24.2	625	1 TBBO	thrombin (EC 3.4.2
22	362.5	23.5	169	2 A40522	thrombin (EC 3.4.2
23	357.5	23.2	618	2 A35827	thrombin (EC 3.4.2
24	351	22.8	622	1 TBHU	thrombin (EC 3.4.2
25	348	22.6	617	2 S10511	thrombin (EC 3.4.2
26	309.5	20.1	562	1 UKHRT	t-plasminogen acti
27	295.5	19.2	559	1 A35029	t-plasminogen acti
28	281.5	18.3	559	1 A29941	t-plasminogen acti
29	278	18.1	120	2 E61545	plasmin (EC 3.4.21

30	271	17.6	89	2 A60140	plasmin (EC 3.4.21
31	268	17.4	123	2 C61545	plasmin (EC 3.4.21
32	241.5	15.7	937	2 A45082	neurotrophic recep
33	240	15.6	943	2 B45082	neurotrophic recep
34	237.5	15.4	946	1 A47299	ror-related recept
35	233	15.1	603	2 S28941	coagulation factor
36	214	13.9	558	2 JC5878	plasma hyaluronan-
37	210	13.6	560	1 JC4795	plasma hyaluronan-
38	201	13.1	291	2 I38098	t-plasminogen acti
39	198	12.9	615	1 KFH12	coagulation factor
40	190.5	12.4	593	2 S45281	coagulation factor
41	188.5	12.2	655	1 A46688	hepatocyte growth
42	178.5	11.6	806	2 T18840	hypothetical prote
43	165	10.7	433	1 JN0560	u-plasminogen acti
44	153	9.9	442	1 UKPS	u-plasminogen acti
45	151	9.8	432	1 S18932	u-plasminogen acti

ALIGNMENTS

RESULT 1
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [mismomer]
N:Contains: angiotatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence, revision 02-Dec-1994 #text change 15-Sep-2000
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625;
R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f
A:Reference number: A35229; MIMD:90202879
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1-810 <PEP>
A:Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA60113.1; PID:9387026
A:Experimental source: leucocyte; lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A:Title: Definition of the transcription initiation site of human plasminogen gene in
A:Reference number: I52242; MIMD:91057523
A:Accession: I52242
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL1>
A:Cross-references: GB:M62890; NID:9190092; PIDN:AAA36454.1; PID:9553613
R:Forstner, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human
A:Reference number: A26646; MIMD:87162450
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: GB:X05199; NID:9355530; PIDN:CAA28831.1; PID:935531
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human a
A:Reference number: I45961; MIMD:85023311
A:Accession: I62738
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

F:79-466/Product: angiotensin #status experimental <AST>
 F:97-560,581-810/Product: plasmin #status experimental <AMT>
 F:97-560/Domains: plasmin chain A #status experimental <CHA>
 F:103-181/Domains: kringle homology <KR1>
 F:185-262/Domains: kringle homology <KR2>
 F:275-352/Domains: kringle homology <KR3>
 F:377-454/Domains: kringle homology <KR4>
 F:481-560/Domains: kringle homology <KR5>
 F:550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 99.7%; Score 1535; DB 1: Length 810;
 Best Local Similarity 99.6%; Pred. No. 7.1e-105;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGKNGTSGTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60
 |||||||
 Db 98 VYLSECKTGNGKNGKNGTSGTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 157
 |||||||
 QY 61 DPGPCWCTTDPKRYDCILCEEECECMHSCGENYDKISTKWSGLECOAMDSQSPH 120
 |||||||
 Db 158 DPGPCWCTTDPKRYDCILCEEECECMHSCGENYDKISTKWSGLECOAMDSQSPH 217
 |||||||
 QY 121 GYPSKPPNNLKKKNGYCRNDRELRCPCFTTDPKRWELCDIPRCTPPSSGPTTCCK 180
 |||||||
 Db 218 GYPSKPPNNLKKKNGYCRNDRELRCPCFTTDPKRWELCDIPRCTPPSSGPTTCCK 277
 |||||||
 QY 181 GTGENYGNVAVTSGTCHQWSAQTPHTERTPEPNCCKNLDENYCRNDGRAPMCHT 240
 |||||||
 Db 278 GTGENYGNVAVTSGTCHQWSAQTPHTERTPEPNCCKNLDENYCRNDGRAPMCHT 337
 |||||||
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 |||||||
 Db 338 TNSQVRWEYCKIPSCDSSPV 357
 |||||||

RESULT 2

B30848
 Plasmin (EC 3.4.21.7) precursor - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C:Accession: B32869; B30848
 R:Tomlinson, J.E.; McLean, J.W.; Lawo, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A:Reference number: A32869; M0ID:89174660
 A:Accession: B32869
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1810 <TOM>
 A:Cross-references: GB:J04697; NID:9342272; PIDN:AAA36901.1; PID:9342273
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-96/Domains: plasminogen-related protein precursor homology <PLPH>
 F:1-9/Domains: signal sequence #status predicted <SIG>
 F:103-181/Domains: kringle homology <KR1>
 F:185-262/Domains: kringle homology <KR2>
 F:275-352/Domains: kringle homology <KR3>
 F:377-454/Domains: kringle homology <KR4>
 F:481-560/Domains: kringle homology <KR5>
 F:581-803/Domains: trypsin homology <TRY>
 F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2: Length 810;
 Best Local Similarity 93.1%; Pred. No. 4.5e-98;
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGKNGTSGTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 60
 |||||||
 Db 98 VYLSECKTGNGKNGKNGTSGTNGITCOKWSSTSPHRRPSPATHPSEGLEENYCRPN 157
 |||||||

QY 61 DPGPCWCTTDPKRYDCILCEEECECMHSCGENYDKISTKWSGLECOAMDSQSPH 120
 |||||||
 Db 158 DPGPCWCTTDPKRYDCILCEEECECMHSCGENYDKISTKWSGLECOAMDSQSPH 217
 |||||||
 QY 121 GYPSKPPNNLKKKNGYCRNDRELRCPCFTTDPKRWELCDIPRCTPPSSGPTTCCK 180
 |||||||
 Db 218 GYPSKPPNNLKKKNGYCRNDRELRCPCFTTDPKRWELCDIPRCTPPSSGPTTCCK 277
 |||||||
 QY 181 GTGENYGNVAVTSGTCHQWSAQTPHTERTPEPNCCKNLDENYCRNDGRAPMCHT 240
 |||||||
 Db 278 GTGENYGNVAVTSGTCHQWSAQTPHTERTPEPNCCKNLDENYCRNDGRAPMCHT 337
 |||||||
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 |||||||
 Db 338 TNSQVRWEYCKIPSCDSSPV 357
 |||||||

RESULT 3

PLPG
 plasmin (EC 3.4.21.7) precursor - pig (fragment)
 N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S03733; S03737; A25834
 R:Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the
 A:Reference number: S03733
 A:Accession: S03733
 A:Molecule type: protein
 A:Residues: 1-560 <SCH>
 R:Brundisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma
 A:Reference number: S03733; M0ID:81212097
 A:Accession: S03737
 A:Molecule type: protein
 A:Residues: 1-57 <BRU>
 R:Marti, T.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen
 A:Reference number: A25834; M0ID:85203907
 A:Accession: A25834
 A:Molecule type: protein
 A:Residues: 450-790 <MAR>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 us the walls of the graafian follicle; also activates the urokinase-type plasminogen
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine pr
 F:1-790/Product: plasminogen #status predicted <PRO>
 F:1-77/Domains: plasminogen-related protein precursor homology (fragment) <PLPH>
 F:1-77/Domains: plasminogen-related protein precursor homology (fragment) <PLPH>
 F:1-77/Domains: activation peptide #status predicted <APV>
 F:78-560/Product: plasmin chain A #status predicted <ACH>
 F:84-162/Domains: kringle homology <KR1>
 F:166-243/Domains: kringle homology <KR2>
 F:256-333/Domains: kringle homology <KR3>
 F:358-435/Domains: kringle homology <KR4>
 F:450-790/Product: miniplasminogen #status experimental <MIN>
 F:461-540/Domains: kringle homology <KR5>
 F:561-790/Product: plasmin chain B #status experimental <BCH>
 F:561-783/Domains: trypsin homology <TRY>
 F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,
 bonds: #status predicted
 F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1: Length 790;
 Best Local Similarity 81.4%; Pred. No. 4e-87;
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYGTMTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
 Db IYLSECKTGNGKRYGTMTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 138
 QY 61 DPGPMCTTDPDKRYDCDILCEECMCHSGENYDGIKSTKMSGLCEOCAMDOSPHAH 120
 Db DEKPMCTTDPDKRYDCDILCEECMCHSGENYDGIKSTKMSGLCEOCAMDOSPHAH 198
 QY 121 GYISKFPNKLKKNYCRNPDRELPRMPCFTTDPNKRWEELCDIPRCCTPPSSGPTQCLK 180
 Db GYISKFPNKLKKNYCRNPDRELPRMPCFTTDPNKRWEELCDIPRCCTPPSSGPTQCLK 258
 QY 181 GTGENTRGNAVAVSGHTCOHWSAQTPHTHERPPENPCNLDENYCRNPDGKRAWCHT 240
 Db GRENTRGVAVSGHTCOHWSAQTPHTHERPPENPCNLDENYCRNPDGKRAWCHT 318
 QY 241 TNSQVRMEYCKIPSCDSS 258
 Db TNSQVRMEYCKIPSCDSS 336
 RE 4
 PL 4
 Plasmin (EC 3.4.21.7) precursor - bovine
 N:Alternate names: plasminogen
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1987 #sequence, revision 28-Apr-1995 #text_change 18-Jun-1999
 R:Accession: S45046; A25835; I45961; S03736
 R:Berghlund, L.; Andersen, M.D.; Petersen, T.E.
 submitted to the EMBL Data Library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BER>
 A:Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
 A:Experimental source: Liver
 A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
 R:Schallier, J.; Moser, P.W.; Danneberger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
 Eur. J. Biochem. 149, 267-278, 1985
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmin
 A:Reference number: A25835; MUID:85203906
 A:Accession: A25835
 A:Molecule type: protein
 A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A:Reference number: I45961; MUID:85023311
 A:Accession: I45961
 A:Note: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 706-743, 'R', 745-812 <MAL>
 A:Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
 R:Brundish, R.A.; Lerch, P.G.; Schallier, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
 A:Reference number: S03735; MUID:81212097
 A:Accession: S03736
 A:Molecule type: protein
 A:Residues: 27-83 <BRU>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen activator
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringe; plasma;
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:8-103/Domain: plasminogen-related protein precursor homology <PLPR>
 F:8-812/Product: plasminogen #status experimental <PRO>
 F:27-103/Domain: activation peptide #status experimental <APT>
 F:104-583, 584-812/Product: plasmin #status experimental <AP>
 F:104-583/Domain: plasmin chain A #status experimental <ACH>

F:110-188/Domain: kringe homology <KR1>
 F:152-269/Domain: kringe homology <KR2>
 F:282-359/Domain: kringe homology <KR3>
 F:384-461/Domain: kringe homology <KR4>
 F:485-564/Domain: kringe homology <KR5>
 F:584-812/Domain: plasmin chain B #status experimental <BCH>
 F:584-805/Domain: trypsin homology <TRY>
 F:56-80, 60-68, 110-188, 131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342
 bonds: #status predicted
 F:315/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:365/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:624, 667, 762/Active site: His, Asp, Ser #status predicted

Query Match 83.8%; Score 1291; DB 1; Length 812;
 Best Local Similarity 80.8%; Pred. No. 4, 9e-87;
 Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKRYGTMTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
 Db IYLSECKTGNGKRYGTMTKNGITCQKWSSTSPHRRPSPATHPSEGLEENYCRNPDN 164
 QY 61 DPGPMCTTDPDKRYDCDILCEECMCHSGENYDGIKSTKMSGLCEOCAMDOSPHAH 120
 Db DENPMCTTDPDKRYDCDILCEECMCHSGENYDGIKSTKMSGLCEOCAMDOSPHAH 224
 QY 121 GYISKFPNKLKKNYCRNPDRELPRMPCFTTDPNKRWEELCDIPRCCTPPSSGPTQCLK 180
 Db GYISKFPNKLKKNYCRNPDRELPRMPCFTTDPNKRWEELCDIPRCCTPPSSGPTQCLK 284
 QY 181 GTGENTRGNAVAVSGHTCOHWSAQTPHTHERPPENPCNLDENYCRNPDGKRAWCHT 240
 Db GTGENTRGNAVAVSGHTCOHWSAQTPHTHERPPENPCNLDENYCRNPDGKRAWCHT 344
 QY 241 TNSQVRMEYCKIPSCDSSPV 260
 Db TNSQVRMEYCKIPSCDSSPV 364

RESULT 5
 PLMS
 Plasmin (EC 3.4.21.7) precursor - mouse
 N:Contants: angiotensin; plasminogen
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1991 #sequence, revision 01-Nov-1996 #text_change 18-Jun-1999
 R:Accession: A38514; S48202; S48203
 R:Degeen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
 Genomics 8, 45-61, 1990
 A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of
 A:Reference number: A38514; MUID:91184812
 A:Accession: A38514
 A:Molecule type: mRNA
 A:Residues: 1-812 <DEG>
 A:Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
 R:Lijnen, H.R.; Van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; MUID:95010076
 A:Accession: S48202
 A:Molecule type: protein
 A:Residues: 20-25 <LIJ>
 A:Accession: S48203
 A:Molecule type: protein
 A:Residues: 22-27 <LIJ>
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
 immediately after dissociation from the clot. In the presence of the inhibitor, the act
 e inhibitor, the activation involves also removal of the activation peptide.
 C:Comment: Stromelysin 1 (see PIR:KCMS1) acts on plasminogen to produce angiotensin.
 eful in treating solid tumors.
 A:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen

RESULT 8
JH0579
hepatocyte growth factor precursor [validated] - human
N:Alternate names: hepatopietin A; scatter factor
C:Species: Homo sapiens (man)
C:Date: 17-Aug-1992 #sequence; revision 17-Aug-1992 #text; change 08-Dec-2000
C:Accession: JH0579; J00333; A41140; B36677; A33512; A39006; PH0114; A37796; S06
R:Seiki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A:Title: Organization of the human hepatocyte growth factor-encoding gene.
A:Reference number: JH0579; MUID:91340155
A:Accession: JH0579
A:Molecule type: DNA
A:Residues: 1-728 <SEK>
A:Cross-references: DBP:D90318
A>Note: The authors translated the codon GAA for residue 662 as Gly
R:Seiki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
submitted to JFID, March 1991
A:Description: Organization of the human hepatocyte growth factor-encoding gene.
A:Reference number: J00333
A:Accession: J00333
A:Molecule type: DNA
A:Residues: 1-481, 'RT', 484-728 <SE2>
R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth f
A:Reference number: A41140; MUID:91334393
A:Accession: A41140
A:Molecule type: mRNA
A:Residues: 1-728 <MET>
A:Cross-references: GB:WJ2339; NID:9337935; PIDN:AA64239.1; PID:9337936
R:Seiki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth facto
A:Reference number: A36677; MUID:91025062
A:Accession: B36677
A:Molecule type: mRNA
A:Residues: 1-728 <SE3>
A:Cross-references: GB:M60718; NID:9184031; PIDN:AA52648.1; PID:9184032
A:Accession: A36677
A:Molecule type: mRNA
A:Residues: 1-161, 167-728 <SE4>
A:Cross-references: EMBL:X1633
A:Experimental source: leukocyte
R:Miyaizawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
A:Reference number: A33512; MUID:89392017
A:Accession: A33512
A:Note: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-728 <MT>
A:Cross-references: GB:M29145; NID:9184041; PIDN:AA52650.1; PID:9184046
R:Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hitt
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A:Reference number: A39006; MUID:91110540
A:Accession: A39006
A:Molecule type: mRNA
A:Residues: 1-161, 167-728 <RUB>
A:Cross-references: GB:M55379
A:Experimental source: embryonic lung
R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A:Title: Identification of the N-terminal residue of the heavy chain of both native and
A:Reference number: PH0114; MUID:91207365
A:Accession: PH0114
A:Molecule type: protein
A:Residues: 32-43; 53-58 <YOS>
R:Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990

A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of
A:Reference number: A37796; MUID:91035621
A:Accession: A37796
A:Molecule type: protein
A:Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X
R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seiki, T.; Shimomishi, M.; Sugimura, A.; Ta
Nature 342, 440-443, 1989
A:Title: Molecular cloning and expression of human hepatocyte growth factor.
A:Reference number: S06794; MUID:90066676
A:Accession: S06794
A:Molecule type: mRNA
A:Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-38
A:Cross-references: EMBL:X16323; NID:932081; PIDN:CAA34387.1; PID:932082
A:Experimental source: liver
A:Note: the authors translated the codon CAG for residue 727 as Glu
R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Bir
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth f
A:Reference number: I59214; MUID:93087571
A:Accession: I59214
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-288, 'ET', <HNR>
A:Cross-references: GB:I02931; NID:9184033; PIDN:AA52649.1; PID:9184034
R:Miyaizawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A:Title: An alternatively processed mRNA generated from human hepatocyte growth facto
A:Reference number: S15443; MUID:91200041
A:Accession: S15443
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-288, 'ET', <MTY2>
A:Cross-references: EMBL:X57574; NID:932083; PIDN:CAA40802.1; PID:932084
R:Shim, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 160, 1151-1158, 1991
A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: clon
A:Reference number: I52253; MUID:92062058
A:Accession: I52253
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 161-166 <SHI>
A:Cross-references: GB:S62561; NID:9237996; PIDN:AA620169.1; PID:9237997
C:Genetics:
A:Gene: GDB:HGF
A:Cross-references: GDB:127524; OMIM:142409
A:Map position: 7q21.1-7q21.1
A:Introns: 30/71, 85/72, 123/71, 161/72, 209/71, 249/72, 289/71, 347/72, 390/71, 424/72, 469/71,
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F:1-31/Domain: signal sequence #status predicted <SIC>
F:33-494/Domain: alpha chain #status predicted <SIC>
F:32-494/Domain: alpha chain #status experimental <ACH>
F:128-206/Domain: kringle homology <KR1>
F:211-288/Domain: kringle homology <KR2>
F:305-383/Domain: kringle homology <KR3>
F:391-469/Domain: kringle homology <KR4>
F:495-728/Domain: beta chain #status experimental <BECH>
F:495-716/Domain: trypsin homology <TRY>
F:32/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status expert
F:294/402: 566, 655/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:487-604/Disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;
Best local Similarity 51.0%; Pred. No. 5; Se-51;
Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;
OY 2 YLSECKTGNGKNYRGTMSTKTRNGITCKWSSSTSPHRRPSPATHPSEGLEENYCRPNPD 61

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      124 YLRNCTIGGRSRTGTVSITKSGIKCPWSSMIPHEHSFLPSSYRGKDLQENCRNPRGE 183
      62 POGPMCTTDPPEKRYDYCDLLECEE-ECMHGSGENTDGKISKTMISGLECAMDSQSPHAA 120
      184 EGGPMCFETSNPEYRVEYCDIPQCSVEECMTGNGESYRGPMHDHESGKICORMDQHPHRR 243
      121 GYIPSKFPMKLNKKNYCRNPDRELPRMCFETTPDNKRKMECLDIPRCL-TPPPSSGP-7Y 176
      244 KFLPERYPDKGFDDNCRNPDGSRPMWCYTLDPTDPTMEXCAIKTCADNTMNDIDVPLETT 303
      177 QCLKGTGENTRGVAVTVSGHTCOHMSAOTPRHTEHPENFPCKNLIDENYCRNPDGKRAP 236
      304 ECIQGGEGEYRGTVNTIMGCIPOQRMDSQYRPHEDMTPEMFCKDLRENYCRNPDGSESP 363
      237 WCHTNSQVMEYC-KIPSCDSS 258
      364 WCETTPDPIRIVGYCSQIPNCDMS 386

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      9
      A35644
      hepatocyte growth factor precursor - rat
      N:Alternate names: hepatoleitin A; scatter factor
      C:Species: Rattus norvegicus (Norway rat)
      C:Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000
      C:Accession: A35644; S13211
      R:Tashiro, K.; Hagiya, M.; Nishitawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamura
      Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
      A:Title: Deduced primary structure of rat hepatocyte growth factor and expression of the
      A:Reference number: A35644; MUID:902219197
      A:Accession: A35644
      A:Status: preliminary
      A:Molecule type: mRNA
      A:Residues: 1-728 <TAS>
      A:Cross-references: GB:D90102; GB:M32987; NID:9220766; PIDN:BA114133.1; PID:9220767
      A:Note: The authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
      R:Okajima, A.; Miyazawa, K.; Kitamura, N.
      Eur. J. Biochem. 193, 375-381, 1990
      A:Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur
      A:Reference number: S13211; MUID:91031482
      A:Accession: S13211
      A:Status: preliminary
      A:Molecule type: mRNA
      A:Residues: 1-728 <OKA>
      A:Cross-references: EMBL:X54400; NID:956353; PIDN:CA38266.1; PID:94539554
      C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
      C:Function:
      A:Description: stimulates mitosis of hepatocytes and other cells
      A:Note: does not have proteinase activity
      C:Superfamily: hepatocyte growth factor; kringe homology; trypsin homology
      C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringe; pyr
      F:1-33/Domain: signal sequence #status predicted <SIG>
      F:56-495/Product: hepatocyte growth factor #status predicted <MAT>
      F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
      F:129-207/Domain: kringe homology <KR1>
      F:212-289/Domain: kringe homology <KR2>
      F:306-384/Domain: kringe homology <KR3>
      F:392-470/Domain: kringe homology <KR4>
      F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
      F:496-719/Domain: trypsin homology <TRY>
      F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
      F:295,403,569,666/Binding site: carbohydrate (Asn) (covalent) #status predicted
      F:488-607/Disulfide bonds: #status predicted

```

```

Query Match          50.8%; Score 782; DB 1; Length 728;
Best Local Similarity 49.8%; Pred. No. 6,9e-50;
Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;

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```

OY 2 YLSECTGKGNKRTGMSKTKNITCQKMSSTSPHPRPSPAHPSBGLSEANTCRPNDD 61
      125 YLRNCTIGGRSRTGTVSITKSGIKCPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 184

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      OY 62 POGPMCTTDPPEKRYDYCDLLECEE-ECMHGSGENTDGKISKTMISGLECAMDSQSPHAA 120
      185 EGGPMCFETSNPEYRVEYCDIPQCSVEECMTGNGESYRGPMHDHESGKICORMDQHPHRR 244
      121 GYIPSKFPMKLNKKNYCRNPDRELPRMCFETTPDNKRKMECLDIPRCL-TPPPSSGP 174
      245 KFLPERYPDKGFDDNCRNPDGSRPMWCYTLDPTDPTMEXCAIKTCADNTMNDIDVPLETT 302
      175 TYQCLGTGENTRGVAVTVSGHTCOHMSAOTPRHTEHPENFPCKNLIDENYCRNPDGKR 234
      303 TTECITGQGEYRGTVNTIMGCIPOQRMDSQYRPHKADITPENFKCDLRENYCRNPDGAE 362
      235 APWCHTNSQVMEYC-KIPSCDSS 258
      363 SPMCFETTPDPIRIVGYCSQIPKCDVS 387

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      RESULT 10
      I51283
      hepatocyte growth factor precursor - clawed frog
      N:Alternate names: hepatoleitin A; scatter factor
      C:Species: Xenopus sp. (Clawed frog)
      C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
      C:Accession: I51283
      R:Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
      Mech. Dev. 49, 123-131, 1995
      A:Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus
      A:Reference number: I51283; MUID:95267690
      A:Accession: I51283
      A:Status: preliminary; translated from GB/EMBL/DBJ
      A:Molecule type: mRNA
      A:Residues: 1-710 <NAK>
      A:Cross-references: GB:S77422; NID:9989932; PIDN:AA34354.1; PID:9989933
      A:Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucle
      C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
      C:Function:
      A:Description: stimulates mitosis of hepatocytes and other cells
      A:Note: does not have proteinase activity
      C:Superfamily: hepatocyte growth factor; kringe homology; trypsin homology
      C:Keywords: duplication; glycoprotein; growth factor; heterodimer; kringe
      F:42-477,478-709/Product: hepatocyte growth factor #status predicted <MAT>
      F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
      F:115-193/Domain: kringe homology <KR1>
      F:198-275/Domain: kringe homology <KR2>
      F:289-367/Domain: kringe homology <KR3>
      F:375-453/Domain: kringe homology <KR4>
      F:478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
      F:478-700/Domain: trypsin homology <TRY>
      F:52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status
      F:470-588/Disulfide bonds: #status predicted

```

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Query Match          50.4%; Score 776.5; DB 1; Length 710;
Best Local Similarity 50.0%; Pred. No. 1,7e-49;
Matches 130; Conservative 39; Mismatches 88; Indels 3; Gaps 3;

```

```

OY 2 YLSECTGKGNKRTGMSKTKNITCQKMSSTSPHPRPSPAHPSBGLSEANTCRPNDD 61
      111 YIRDCJHGKSNYRGTRNTRKGLACOPWNSMIPHEHSFLPSTYRKDKLENYCRNPRKE 170
      62 POGPMCTTDPPEKRYDYCDLLECEE-ECMHGSGENTDGKISKTMISGLECAMDSQSPHAA 120
      171 EGGPMCFETSNPEYRVEYCDIPQCSVEECMTGNGESYRGPMHDHESGKICORMDQHPHRR 230
      121 GYIPSKFPMKLNKKNYCRNPDRELPRMCFETTPDNKRKMECLDIPRCL-TPPPSSGPYQCL 179
      231 KFLPERYPDKGFDDNCRNPDGSRPMWCYTLDPTDPTMEXCAIKTCADNTMNDIDVPLETT 290
      180 KGTGENTRGVAVTVSGHTCOHMSAOTPRHTEHPENFPCKNLIDENYCRNPDGKRAPWCH 239
      291 KGGEGEYRGSTVSYTYNGICQQRMDSQFPHLHNTPENYRKCKDLENYCRNPDGSESPWCF 350

```

oy 240 TTN5OVRMEYC-KRPSCDS 258
11 : - : - : - : - :
Db 351 TTDPNIRIGHCSQIKKCOAS 370

RESULT 11
A60185
hepatocyte growth factor precursor - mouse
N.Alternate names: hepatolietin A; scatter factor
C.Species: Mus musculus (house mouse)
C.Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
C.Accession: JG2117, PC2064; A60185; S43416; S45521; SLI7173; SI0966; I48758; JU0231
R.Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A.Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep
A.Reference number: JC2117, MUID:94183257
A.Accession: JC2117
A.Molecule type: mRNA
A.Residues: 1-728 <SAS>
A.Cross-references: GB:D10212; NID:g220435; PIDN:BAA01064.1; PID:g220436
A.Experimental source: Fibroblast, COS-1 cell
A.Submission: submitted to JUPID, May 1993
A.Accession: PC2064
A.Molecule type: protein
A.Residues: 496-504 <SAD>
R.Rosen, E.M.; Meromsky, L.; Setter, E.; Winter, D.W.; Goldberg, I.D.
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
A>Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig
A.Reference number: A60185; MUID:90377927
A.Accession: A60185
A.Molecule type: protein
A.Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,'E',379,
R.Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
A>Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A.Reference number: S43416; MUID:94060105
A.Accession: S43416
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-728 <LIU>
A.Cross-references: EMBL:X72307
R.Liu, Y.
submitted to the EMBL Data Library, May 1993
A.Reference number: S45521
A.Accession: S45521
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-563,'H',565-728 <LI2>
A.Cross-references: EMBL:X72307
R.Berger, A.; Fellous, J.; Young, S.; Pappin, D.; Rahman, D.
Biol. J. 278, 35-41, 1991
A>Title: Purification and characterization of biologically active scatter factor from re
A.Reference number: SLI7173; MUID:91354223
A.Accession: SLI7173
A.Molecule type: protein
A.Residues: 496-517,'T',519 <COF>
R.Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A>Title: Hepatocytes and scatter factor.
A.Reference number: SI0966; MUID:90326152
A.Accession: SI0966
A.Status: preliminary
A.Molecule type: protein
A.Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
R.Platschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A>Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A.Reference number: I48758; MUID:95122532
A.Accession: I48758
A.Status: preliminary
A.Molecule type: DNA
A.Submission: translated from GB/EMBL/DDBJ
A.Residues: 1-30 <RES>
A.Cross-references: EMBL:X81630; NID:g673451; PIDN:CMA57286.1; PID:g673452

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F:1-32/Domain: signal sequence #status predicted <SIG>
F:56-495/Domain: hepatocyte growth factor #status predicted <MAT>
F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:129-207/Domain: kringle homology <KR1>
F:212-289/Domain: kringle homology <KR2>
F:306-384/Domain: kringle homology <KR3>
F:392-470/Domain: kringle homology <KR4>
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F:496-719/Domain: trypsin homology <TRY>
F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:295/403,565/556/Binding site: carboxydate (Asn) (covalent) #status predicted
F:488-607/Disulfide bonds: #status predicted

Query Match	50.4%;	Score 776;	DB 1;	Length 728;
Best Local Similarity	49.4%;	Pred. No. 1.9e-49;		
Matches 131;	Conservative	40;	Mismatches	.84;
			Indels	10;
			Gaps	4;

```

0Y 2 YLSECKTNGNGKKRYRSTKTKNGIKCQWSTSPHRRPFSFATPSPGSEBNCRNPDND 63
Db 125 YIRNCLITGKGSYKCTVTSITSGIKCQWMSMITHENSFLRSPSRGKDLDGENTCRNPRGE 164
0Y 62 PQGPMCVTTDPPEKRYDYCDILECEB--ECMHCSGENYDGIKSTNGLSECOAMDQSOPHAH 120
Db 185 EGGPFCFTSNPEVREYEDIQCSSEVECMTCNGESYRPMHNTGSKTCORMDOOTPRH 244
0Y 121 GYIPKPEPNKNLKKKKYCNPNRDELRCWCFETTPDKRMWELDIPRCT-----PPRPSGR 174
Db 245 KFLPRRYDKGFDNDNYCANNPQGRPRWCYTLDPTDPRMYCAIKKCAISAYNEIDVPIHE-- 302
0Y 175 TYOCLKGTGENYRCNVAATVSAGHTCQAHMSAOTPHTHEPTRENPFCKNLDEYCNCRNPDGR 234
Db 303 TTECIQGGEGEGRGTSNTIWMGIRPCQRMWDSQYRPHKHDTITPENFKCKDLRENYCNRNPDGA 362
0Y 235 APMCHTINSOVRMEYC-KIPSCDSS 258
Db 363 SPWCFETTPDNLRVGCSQIPKCDVS 387

```

RESULT 12

macrophage-stimulating protein 1 precursor - rat
JC5061

C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1997 #sequence_revision 16-Jun-2000
C:Accession: JC5061

R:Ohnishi, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasawa
Biochem. Biophys. Res. Commun. 227, 273-280, 1996

A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement
A:Reference number: JC5061; MUID:97011126

A:Accession: JC5061

A:Molecule type: mRNA

A:Residues: 1-716 <OHSS>

A:Cross-references: EMBL:X55096; NID:q1669718; PIDN:CA664473.1; PID:q1669719

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: duplication; glycoprotein; growth factor; kringle

F:1-31/Domain: signal sequence #status predicted <SIG>
F:332-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F:332-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
F:110-186/Domain: kringle homology <KR1>
F:191-268/Domain: kringle homology <KR12>
F:292-370/Domain: kringle homology <KR13>
F:379-457/Domain: kringle homology <KR14>
F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
F:489-709/Domain: trypsin homology <TRY>
F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible]

```

RESULT 13
151285
hepatocyte growth factor/scatter factor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 151285
R:Streitl, A.; Sten, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherardo, S.
Development 121, 813-824, 1995
A:Title: A role for HGF/SF in neural induction and its expression in Hensen's node during
A:Reference number: 151285; MUID:95237013
A:Accession: 151285
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-411 <STR>
A:Cross-references: GB:S77480; NID:g998675; PID:g998676
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
F:124-197/domain: kringle homology <KR2>
F:202-279/domain: kringle homology <KR2>
F:296-374/domain: kringle homology <KR3>

```

Match	49.0%	Score 754.5	DB 2	Length 411
Local Similarity	50.2%	Pred. NO. 4e-48		
Matches 132; Conservative	31;	Mismatches	89;	Indels 11; Gaps 4

[illegible]

RESULT 14

A40332
macrophage-stimulating protein 1 precursor - mouse
N:Alternate names: hepatocyte growth factor-like protein
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence-Revision 17-Jul-1992 #text-change 18-Jun-1999
C:Accession: A40332; B40332
R:Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A:Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth f
A:Reference number: A40332; MUID:92002017
A:Accession: A40332
A:Molecule type: DNA
A:Residues: 1-716 <DECG>
A:Cross-references: GB:M74180; NID:g193831; PIDN:AAA50166.1; PID:g193832
A:Accession: B40332
A:Molecule type: mRNA
A:Residues: 1-118, 'P', 20-716 <DECG2>
A:Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C:Genetics:
A:Introns: 18/1: 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1;
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: duplication; glycoprotein; growth factor; kringle
F:1-31/Domains: signal sequence #status predicted <SIG>
F:19-488, 488-716/Product: macrophage-stimulating protein 1 #status experimental <MATH>
F:19-483/Domains: alpha chain #status experimental <ACH>
F:110-186/Domains: kringle homology <KR1>
F:191-268/Domains: kringle homology <KR2>
F:292-370/Domains: kringle homology <KR3>
F:379-457/Domains: kringle homology <KR4>
F:484-711/Domains: beta chain #status experimental <BCH>
F:489-709/Domains: trypsin homology <TRY>
F:72, 173, 305, 620/Binding site: carboxylate (Asn) (covalent) #status predicted

	Query Match	48.9%	Score 753.5	DB 1:	Length 716:	
	Best Local Similarity	48.3%	Pred. No. 8.2e-48:			
	Matches 129;	Conservative	37;	Mismatches 86;	Indels 15;	Gaps 5
Qy	2 YLSEKTKGNGKNYROTMSKTNGITCQKMSSTSPHPRFSPAHPDTHPSEGLEENYCRRPND	61	:	:	:	:
Dd	106 YRRTIMDNQVSYRGTVARTAGGLCCQAMSRFRPDHKTPPL--PKNGLEEFRCRRPDD	163	:	:	:	:
Qy	62 PGGPCYTTDPDEKRYDYCDILECEE--CMHGSGENYDKGISKTMSGLEGCQANDSOPNAH	120	:	:	:	:
Dd	164 PRGPWCYTNNRSVRFROSCGIKTCREAVCYLCAGEDVRGEVDVTESGRECGRMIDLPHSH	223	:	:	:	:
Qy	121 GYIPSKFPNKLNKKNYCRNPDRBLRPWCFETTDPNKRWEIJDIPRC--TTPP-----	170	:	:	:	:
Dd	224 PROPKEFLDKDLKDWNCRRNPDSDSERPMWCTTDPNVEREFCDCLPSCGNLPATVKGSKSOR	283	:	:	:	:
Qy	171 -SSGPTTYOCLKGTGENYRKANNAVYYSGHCQQMNSAQTPIHTHERTEPNFCKNLUDENYCN	229	:	:	:	:
Dd	284 RNKGALNCFNRKGGEDYRETNTWTSGVPCQWDASPOHHRFVPEKYACKDLREKFCRN	343	:	:	:	:
Qy	230 PDGRAPMCCHTINSOVAMEYC-KIPSC	255	:	:	:	:
Dd	344 PDGSEAPMCFTRPGILRAAFCHQIDPRC	370	:	:	:	:

RESULT 15
S00657
apolipoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N:Alternate names: apolipoprotein(a); Lipo(a) chain apo(a)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A42233; I52415; I65286
R:McLean, J.W.; Tomlinson, J.E.; Kiang, W.J.; Becton, D.L.; Chen, E.Y.; Fleiss, G.M.;
Nature 330, 133-137, 1987
A:File: cdna sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; MUID:88039109

A;Molecule type: mRNA

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